



# 中国小菜蛾群体遗传变异的时空动态

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**摘要:**【目的】小菜蛾 *Plutella xylostella* 是十字花科蔬菜最重要的迁移性害虫之一, 在中国越冬区 (OR) 的群体和季节性繁殖区 (SBR) 的群体之间具有“源-汇”关系和复合群体的特征。本研究旨在揭示中国小菜蛾群体遗传变异的时空动态, 以期进一步阐明该虫的迁移特性及其对区域灾变的影响。【方法】基于已经发表的 4 组不同采样时间中国小菜蛾 *COI* 序列 (共 1 567 条) 数据, 将每个数据集细分为 3 组: OR 群体、SBR 群体以及特定采样时间 (ST) 的群体。对不同组 (群体) 进行遗传多样性、遗传分化、单倍型相似性和群体演化史的分析。【结果】基于 *COI* 序列的小菜蛾群体遗传变异分析结果表明, 同一采样时间内, OR 群体和 SBR 群体遗传多样性水平相当。虽然 SBR 群体在单倍型频率上不稳定, 导致包含 SBR 的群体间遗传分化较大, 但 SBR 群体单倍型均能够在同一采样时间的 OR 群体中找到, 或 SBR 单倍型仅与 OR 单倍型相差 2 个碱基以内; SBR 群体中单倍型频率在不同年份间变化大, 遗传分化最大, 而 ST 群体之间遗传分化的变异水平最低。不同采样时间样品 *COI* 序列的碱基错配分布图呈现相同的单峰状, 且不同采样时间样本主要是由几种相同的单倍型构成。【结论】这些结果表明: 迁移是影响中国季节性繁殖区小菜蛾群体遗传变异的主要因素; 中国不同区域的小菜蛾群体遗传变异在时间尺度上具有稳定性和相关性。小菜蛾复合群体特征为阐明其季节性迁移特性提供了重要的生态学依据。

**关键词:** 小菜蛾; 时空尺度; 遗传变异; 迁移; 越冬区; 季节性繁殖区

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## Spatiotemporal dynamics of genetic variation in populations of the diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae), in China

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**Abstract:** 【Aim】The diamondback moth, *Plutella xylostella* L., is one of the most important dispersal pests of cruciferous vegetables worldwide, and it is featured by the interrelated metapopulations of “source-sink” between overwintering regions (OR) and seasonally breeding regions (SBR) in China. This study aims to investigate the spatiotemporal dynamics of genetic variation in *P. xylostella* populations

in China and to further uncover the effect of dispersal behavior on its regional outbreaks. 【Methods】 The genetic variation of *P. xylostella* populations was investigated based on four independent datasets of 1 567 *COI* sequences of *P. xylostella* at different sampling time in China. Each dataset was classified into three groups, *i. e.*, OR populations, SBR populations and populations sampled at a given sampling time (ST). The genetic diversity, genetic differentiation, haplotype similarity and demography history of these populations were investigated. 【Results】 Genetic variation analysis of *P. xylostella* populations based on *COI* sequences revealed a comparable genetic variation between OR and SBR populations sampled at the same time. Although the unstable haplotype frequency in SBR led to a great genetic differentiation of SBR-involved populations, *COI* haplotypes in SBR populations either could be found in OR populations sampled at the same time or showed a limited difference ( $< 2$  bp) from the *COI* haplotypes in OR populations. The haplotype frequency of SBR populations varied greatly among different years. Variation of genetic differentiation between SBR populations was the highest in all population combinations, while that between ST populations was the lowest. Haplotype analysis at different sampling time showed a similar pattern in nucleotide mismatch distributions, and the similar haplotype pattern consists of several dominant haplotypes. 【Conclusion】 Our results indicate that dispersal is the major factor in shaping the genetic variation of SBR populations of *P. xylostella*, and *P. xylostella* populations tend to exhibit a temporal stability and interrelation of genetic variation in different regions of China. The nature of metapopulation provides an important ecological base for understanding the seasonal dispersal of *P. xylostella*.

**Key words:** *Plutella xylostella*; spatiotemporal scale; genetic variation; dispersal; overwintering region; seasonally breeding region

遗传变异是维持群体在变化环境中稳定性的重要因素 (Lacy, 1997; Frankham *et al.*, 2010; Kirk and Freeland, 2011)。解析群体遗传结构及其影响因素是进化生态学研究的重要内容,在保育生物学、动植物育种和害虫防治受到广泛的关注 (Tabachnick, 1992; Frankham *et al.*, 2010; Muñoz *et al.*, 2017; Varella *et al.*, 2017)。对害虫群体遗传格局的解析有助于了解其群体迁移及基因流的时空动态,是制定有效害虫防治策略的关键 (Tabachnick, 1992; Wei *et al.*, 2013)。

小菜蛾是十字花科蔬菜最重要的害虫之一 (Shelton, 2001),在全世界 140 多个国家和地区有记录和报道 (<https://www.cabi.org/isc/datasheet/42318>)。它可借助气流从越冬区 (overwintering region, OR) 迁往季节性繁殖区 (seasonally breeding region, SBR) (Honda, 1990; Chapman *et al.*, 2002; Dossdall *et al.*, 2004; Fu *et al.*, 2014),但至今鲜有回迁的报道。越冬区的温度处于小菜蛾的适生温度范围内,小菜蛾能够周年繁衍;而季节性繁殖区的小菜蛾群体每年冬季会全部消亡,来年新的群体由越冬区迁入定殖形成 (马春森等, 2010; Wei *et al.*, 2013; Fu *et al.*, 2014)。源-汇群体在时间和空间上

“定殖-消亡-定殖”的过程形成了复合群体特有的群体动态 (Hanski, 1998; Gaggiotti and Hanski, 2004),并通过影响复合群体固有遗传变异 (standing genetic variation) 进一步影响其微进化过程 (Pannell and Charlesworth, 2000)。越冬区和季节性繁殖区的小菜蛾群体之间具备复合群体特性,对其遗传变异时空动态的研究有助于了解这两个区域之间的群体动态,并将利于了解群体迁移及其区域灾变的影响 (Caprio and Hoy, 1994; Fountain *et al.*, 2014)。目前,小菜蛾群体遗传变异在不同空间尺度上受到广泛的关注,从区域尺度的研究 (Kim *et al.*, 1999; Niu *et al.*, 2014; Ke *et al.*, 2015) 到全球范围的解析 (Pichon *et al.*, 2006; Roux *et al.*, 2007; Juric *et al.*, 2017) 表明迁移对于其群体遗传变异具有重要的塑造作用。但到目前为止,鲜有从时间尺度探讨小菜蛾遗传变异的变化情况。

中国的小菜蛾群体分布在越冬区和季节性繁殖区内,是研究复合群体时空动态的理想群体。本研究利用不同采样时间的中国小菜蛾群体遗传数据 (Li *et al.*, 2006; Wei *et al.*, 2013; Yang *et al.*, 2015; 黄素梅, 2015),用于解析其遗传变异在时空尺度的变化情况及相关的影响因子。我们在分析小

菜蛾群体遗传变异时空动态的基础上,探讨了影响越冬区和季节性繁殖区遗传变异的主要因素,旨在阐明小菜蛾群体迁移与季节性繁殖区群体遗传变异的相关性,为我国小菜蛾的区域性防控提供理论指导。

1 材料与方法

1.1 中国小菜蛾群体线粒体 COI 基因序列数据

获取中国小菜蛾群体遗传研究原始的 COI 基因序列数据,包括 Li 等(2006), Wei 等(2013), Yang 等(2015)和黄素梅(2015)。这几组数据独立分析的结果都表明,中国小菜蛾群体不存在遗传结构,因此将这几组数据按照采样时间段(sampling time, ST)划分为 4 个群体: Li, Wei, Yang 和 Huang,即每组数据作为一个群体。根据 Fu 等

(2014)对于小菜蛾越冬区的划分,进一步将小菜蛾群体划分为越冬区(OR)(纬度小于 30°N),混合区(hybrid region, HR)(纬度大于 30°N 小于 35°N)和季节性繁殖区(SBR)(纬度大于 35°N),其中由于 HR 区群体无法确认是否可越冬的状态,因此不用做后续的群体分析。越南的一个群体(黄素梅, 2015)和韩国的两个群体(Li *et al.*, 2006)与中国群体有频繁的基因交流,相似性高,因而分别归于 OR 和 SBR 区,用于群体遗传分析。采用 MEGA 7 (Kumar *et al.*, 2016)中的 Muscle 进行序列比对,截取 COI 基因等长的 516 bp 序列用于群体遗传分析。共有 1 567 条 COI 序列用于后续的研究,其中 Li 80 条,Wei 794 条,Yang 406 和 Huang 287 条。OR 区中 Li 40 条,Wei 321 条,Yang 147 条和 Huang 137 条; SBR 区中 Li 30 条,Wei 263 条,Yang 205 条和 Huang 76 条(表 1)。

表 1 用于本研究的小菜蛾 COI 序列  
Table 1 A summary of COI sequences of *Plutella xylostella* used in this study

| 数据集<br>Dataset | 群体数量<br>Number of<br>populations | 个体数量<br>Number of<br>individuals | 采样时间<br>Sampling<br>time | 自定义群体(个体数)<br>Defined population<br>(number of individuals) | 参考文献<br>References        |
|----------------|----------------------------------|----------------------------------|--------------------------|-------------------------------------------------------------|---------------------------|
| Li             | 8                                | 80                               | 2004                     | SBR (30)                                                    | Li <i>et al.</i> , 2006   |
|                |                                  |                                  |                          | OR (40)                                                     |                           |
|                |                                  |                                  |                          | ST (80)                                                     |                           |
| Wei            | 27                               | 794                              | 2010 – 2011              | SBR (263)                                                   | Wei <i>et al.</i> , 2013  |
|                |                                  |                                  |                          | OR (321)                                                    |                           |
|                |                                  |                                  |                          | ST (794)                                                    |                           |
| Yang           | 18                               | 406                              | 2011                     | SBR (205)                                                   | Yang <i>et al.</i> , 2015 |
|                |                                  |                                  |                          | OR (147)                                                    |                           |
|                |                                  |                                  |                          | ST (406)                                                    |                           |
| Huang          | 25                               | 287                              | 2012 – 2014              | SBR (76)                                                    | 黄素梅, 2015                 |
|                |                                  |                                  |                          | OR (137)                                                    |                           |
|                |                                  |                                  |                          | ST (287)                                                    |                           |

SBR, OR 和 ST 分别指季节性繁殖区群体、越冬区群体和特定采样时间的群体。SBR, OR and ST represent populations from seasonally breeding region, populations from overwintering region and populations sampled at a given sampling time, respectively.

1.2 群体遗传变异分析

将按照区域和时间划分的 12 个群体(表 1)用于遗传多样性分析。首先,计算不同群体的单倍型数量  $N_h$ 、单倍型多样性  $H_d$  和核苷酸多样性  $N_d$ ;其次,在每个采样时间的群体(ST)中随机有放回取 20 头个体,重复取得 1 000 次,计算单倍型数量  $N_h$ 、单倍型多样性  $H_d$  和核苷酸多样性  $N_d$ ;多样性采用 R 中的 pegas 包(Paradis, 2010)进行计算。采用 R (Team R Development Core, 2012)进行遗传多样性与采样时间和样本量的斯皮尔曼秩相关检验。Hedrick’s  $G_{ST}$  (Hedrick, 2005)是独立于遗传多样性的遗传分化参数,因此采用 R 包 mmod (Winter,

2012)计算不同群体之间遗传分化水平 Hedrick’s  $G_{ST}$ ,用于比较不同区域(如 OR-OR 和 SBR-SBR)群体遗传分化的差异。

1.3 群体演化史分析

采用 Dnasp (Librado and Rozas, 2009)计算各个群体的 Tajima’  $D$  和 Fu’  $F_s$  参数,同时构建每一个群体碱基错配图(mismatch distribution),用于分析其演化史。

1.4 单倍型分析

采用韦恩图比较不同采样时间样本单倍型组成的异同。构建不同采样时间(ST)群体以及同一采样时间不同区域(OR 和 SBR)群体的单倍型网络

图,查看不同区域和年份 *COI* 单倍型频率的变化。采用 POPART(Leigh and Bryant, 2015)用于单倍型网络图的构建。

2 结果

2.1 中国小菜蛾群体遗传变异

小菜蛾的遗传多样性分析表明,不同采样时间的群体遗传多样性差异较大。其中,单倍型数量 Huang > Wei > Yang > Li;单倍型多样性 Wei > Huang > Li > Yang;而核苷酸多样性则是 Huang > Wei > Li > Yang。总体来看,Wei 和 Huang 两个采样时间的群体

在单倍型数量、单倍型多样性和核苷酸多样性上都大于 Li 和 Yang(图 1,表 2)。而在同一采样时间的越冬区和季节性繁殖区群体之间,核苷酸多样性、单倍型数量和单倍型多样性上均无明显的差异(表 2)。基于相关性分析发现采样时间和样本数量与遗传变异并没有显著的相关性(斯皮尔曼秩检验, $P>0.05$ )。

在基于不同时间和区域的遗传分化分析中,不同采样时间(ST-ST)遗传分化的变异程度最小,其次是越冬区群体(OR-OR)之间,而在包含有季节性繁殖区(SBR)群体的组合内,群体间遗传分化的变异较大(图 2)。

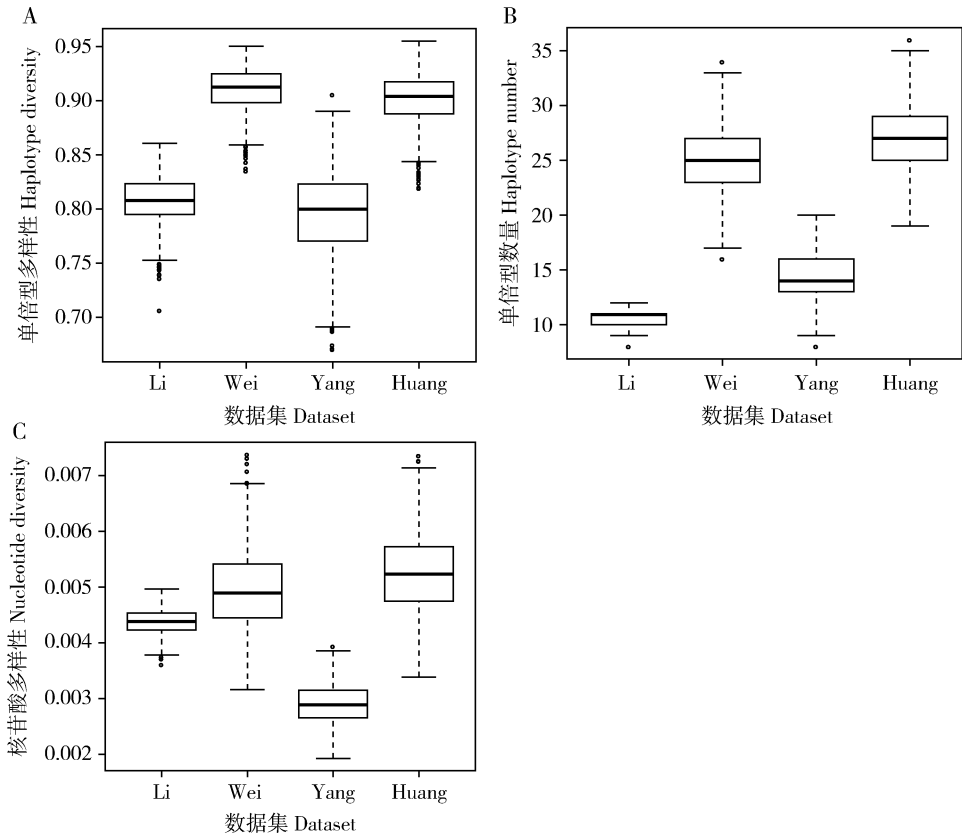


图 1 不同采样时间小菜蛾群体的遗传多样性  
Fig. 1 Genetic diversity of *Plutella xylostella* populations sampled at different time  
A: 单倍型多样性 Haplotype diversity; B: 单倍型数量 Haplotype number; C: 核苷酸多样性 Nucleotide diversity. Li, Wei, Yang 和 Huang 分别表示基于小菜蛾 *COI* 序列的 4 个数据集;下同。从每个群体中有放回取样,每次取 20 头个体,重复取 1 000 次,并进行遗传多样性的计算。Li, Wei, Yang, and Huang represent four *COI* datasets of *P. xylostella*, respectively. The same below. Twenty individuals from each group were sampled with replacement with 1 000 replicates and used for genetic diversity calculation.

| Table 2 Genetic diversity and demographic parameters of <i>Plutella xylostella</i> populations |        |        |            |             |            |            |            |            |        |             |            |            |
|------------------------------------------------------------------------------------------------|--------|--------|------------|-------------|------------|------------|------------|------------|--------|-------------|------------|------------|
|                                                                                                | Li_OR  | Li_SBR | Wei_OR     | Wei_SBR     | Yang_OR    | Yang_SBR   | Huang_OR   | Huang_SBR  | Li     | Wei         | Yang       | Huang      |
| <i>NI</i>                                                                                      | 40     | 30     | 321        | 263         | 147        | 205        | 137        | 76         | 80     | 794         | 406        | 287        |
| <i>Nd</i>                                                                                      | 0.0035 | 0.0038 | 0.0052     | 0.0053      | 0.0033     | 0.0026     | 0.0052     | 0.0057     | 0.0044 | 0.0050      | 0.0029     | 0.0053     |
| <i>Nh</i>                                                                                      | 7      | 7      | 67         | 88          | 21         | 22         | 55         | 41         | 12     | 153         | 27         | 95         |
| <i>Hd</i>                                                                                      | 0.74   | 0.78   | 0.93       | 0.91        | 0.85       | 0.78       | 0.91       | 0.94       | 0.83   | 0.93        | 0.81       | 0.92       |
| Fu's <i>Fs</i>                                                                                 | -0.34  | -0.49  | -77.26 *** | -135.72 *** | -11.91 *** | -15.11 *** | -69.10 *** | -45.93 *** | -1.99  | -294.11 *** | -17.46 *** | -34.40 *** |
| Tajima's <i>D</i>                                                                              | 0.44   | 0.87   | -1.97 *    | -2.13 **    | -0.86      | -1.20      | -2.15 **   | -1.82 *    | -0.19  | -2.18 **    | -1.02      | -2.23 **   |

*NI*: 个体数量 Number of individuals; *Nd*: 核苷酸多样性 Nucleotide diversity; *Nh*: 单倍型数量 Number of haplotypes; *Hd*: 单倍型多样性 Haplotype diversity.  
\*  $P<0.05$ ; \*\*  $P<0.01$ ; \*\*\*  $P<0.001$ .

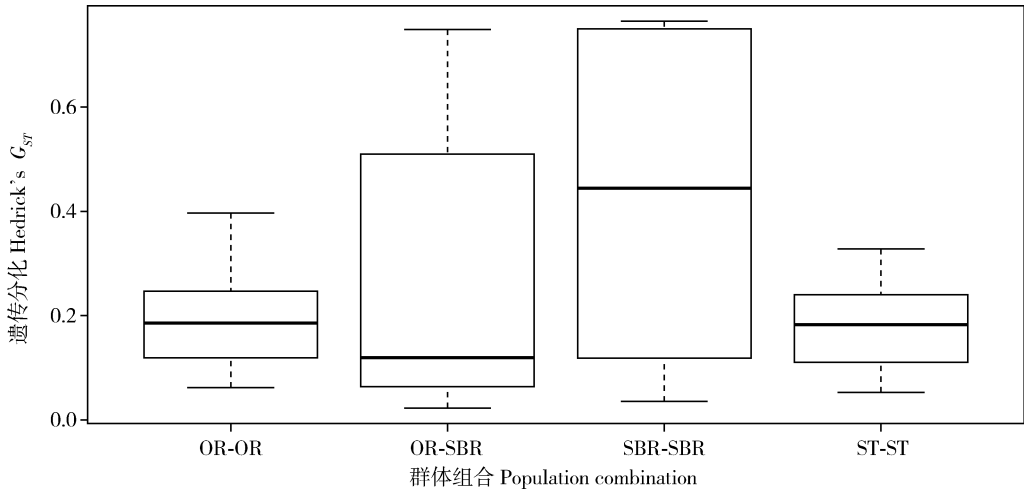


图2 不同小菜蛾群体组合遗传分化分析

Fig. 2 Genetic differentiation of different population combinations of *Plutella xylostella*

ST, OR 和 SBR 分别表示特定采样时间群体、越冬区群体和季节性繁殖区群体。ST, OR and SBR indicate populations sampled at a given sampling time, populations from overwintering region and populations from seasonally breeding region, respectively.

2.2 中国小菜蛾群体演化史

通过演化史分析可以发现,除了 Li 群体之外, Fu's  $F_s$  参数在不同群体内均为负值,表明群体正在经历扩张。对于 Wei 和 Huang 两个群体的 Tajima's  $D$  的分析也支持了同样的结论(表 2)。在

错配分析中,不同采样时间均展示一个相同的格局,即单倍型碱基的差异数集中在 5 以内,表明群体内个体间分化程度低,群体单倍型组成相似,群体内的单倍型是由一种或几种相似的单倍型演化形成的(图 3)。

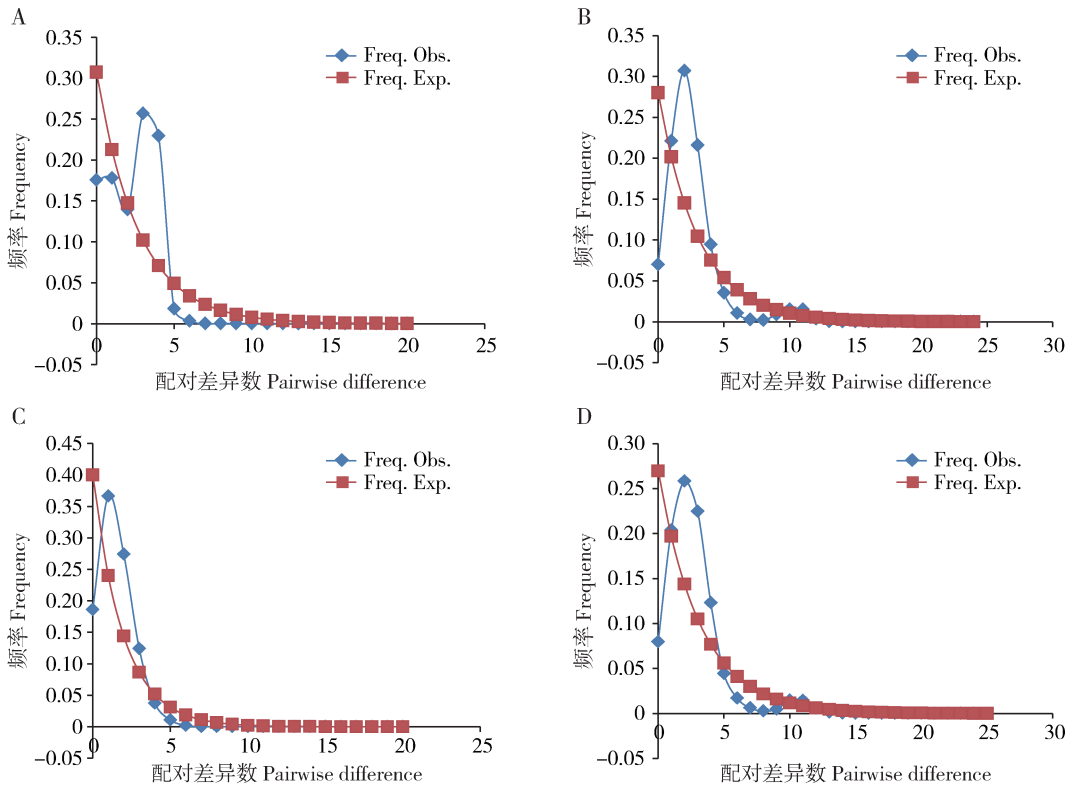


图3 不同采样时间小菜蛾群体的碱基错配分布

Fig. 3 Mismatch distribution of *Plutella xylostella* populations sampled at different time

A: Li; B: Wei; C: Yang; D: Huang. Freq. Obs.: 观测频率 Observed frequency; Freq. Exp.: 期望频率 Expected frequency.

2.3 中国小菜蛾 *COI* 单倍型

通过单倍型网络图和韦恩图可以看出,不同采样时间群体之间主要单倍型 (Hap\_11, Hap\_3 和 Hap\_4)一致 (图 4)。但在特异的单倍型上有较大的差异 (图 4),如 Wei 具有时间特异单倍型数量达到 109 个,Huang 中则有 53 个,而 Li 和 Yang 则分别只有 4 个和 2 个,但这些采样时间特异的单倍型主

要为低频的单倍型 (图 4)。

在同一个采样时间内,SBR 区的单倍型均可以在南方 OR 区中找到,或者与同一采样时间 OR 区的单倍型相差 1~2 个碱基 (图 5)。可以推断中国北方的小菜蛾主要来自于南方,且在不同年份间这一格局较为稳定。

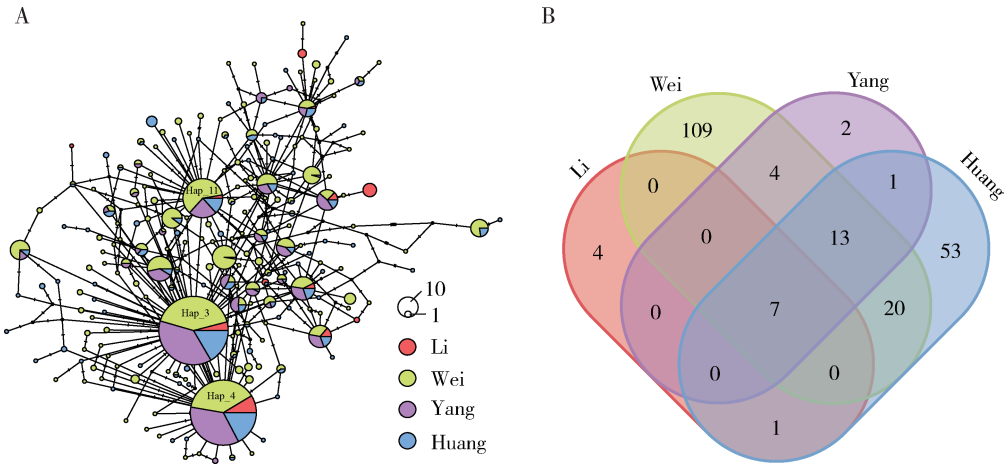


图 4 不同采样时间小菜蛾群体 *COI* 单倍型的特征分析  
Fig. 4 Characteristics of *COI* haplotype of *Plutella xylostella* populations sampled at different time

A: 单倍型网络图 Haplotype network; B: 单倍型韦恩图 Venn plot of haplotypes. 每个圈表示一种单倍型,单倍型间划线数量表示碱基变化的次数,每种单倍型中不同颜色的面积分别表示不同采样时间个体所占的比例。Each circle represents a haplotype. Number of the hatch marks indicates mutation steps between two haplotypes. Areas of different color in each haplotype indicate proportions of individuals from four sampling time, respectively.

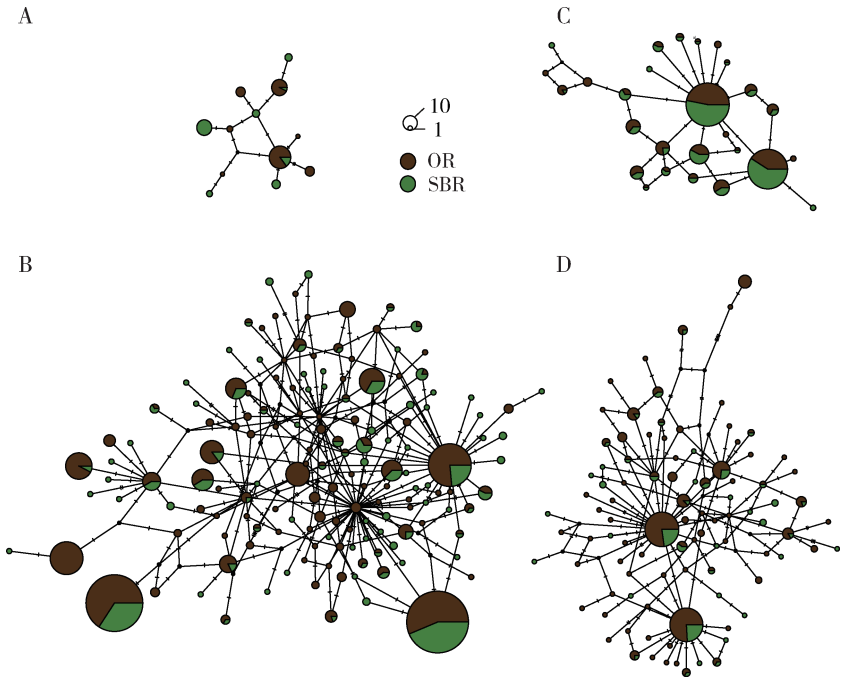


图 5 同一采样时间越冬区 (OR) 和季节性繁殖区 (SBR) 小菜蛾群体 *COI* 序列的单倍型网络图  
Fig. 5 Haplotype network of *COI* sequences of *Plutella xylostella* populations from overwintering region (OR) and seasonally breeding region (SBR) sampled at the same time

A: Li; B: Wei; C: Yang; D: Huang. 每个圈表示一种单倍型,单倍型间划线数量表示碱基变化的次数;每种单倍型中棕色和绿色的面积分别表示越冬区和季节性繁殖区个体所占的比例。Each circle represents a haplotype. Number of the hatch marks indicates mutation steps between two haplotypes. Brown and green areas of each haplotype indicate proportions of individuals from OR and SBR, respectively.

### 3 讨论

#### 3.1 越冬区小菜蛾的群体遗传变异

越冬群体具有连续的世代以及稳定传递的遗传物质,因而其群体遗传变异在时间尺度上较为稳定。小菜蛾在中国纬度小于 30°N 的地区能够越冬(马春森等, 2010; Fu *et al.*, 2014),与这个区域群体遗传变异的稳定性以及年份间遗传分化较小的结果是相吻合的。稳定的遗传变异对于群体的演化以及应对新的环境变化有重要的作用(Mitchellolds and Schmitt, 2006; Varella *et al.*, 2017; Venugopal and Dively, 2017),同时也有助于适应性遗传变异的积累和传递(Tran *et al.*, 2007)。总体来说,由于有越冬区源群体的存在,中国小菜蛾复合群体形成了稳定的遗传变异,并不断增加新的遗传变异(如新 *COI* 单倍型产生);同时小菜蛾本身具备的高年世代数、繁殖力以及杂合基因组的特性,也有利于小菜蛾群体积累遗传变异,并成为其适应性的遗传基础(You *et al.*, 2013)。由于全球气候变暖而导致的小菜蛾越冬北限的北移,将有助于区域小菜蛾群体新遗传变异的形成和积累,这将有可能提高小菜蛾抗药性和区域的致害水平。

#### 3.2 季节性繁殖区小菜蛾的群体遗传变异

从单倍型的网络图可以看出,同一采样时间内小菜蛾在越冬区(“源”)与季节性繁殖区(“汇”)的群体间单倍型碱基差异小,说明两个区域群体之间的“源-汇”关系,即季节性繁殖区的汇群体是由越冬区的源群体迁入的。但由于单倍型频率差异较大,使得不同区域内群体遗传分化较大。时间尺度上的遗传变异表明越冬区和季节性繁殖区小菜蛾群体之间存在稳定的基因交流,群体迁移是影响遗传变异时空格局的重要因素,迁移的随机性则决定了季节性繁殖区群体与越冬区群体在单倍型频率的差异。这一遗传格局与其他具有远距离迁移特性的物种(如黑脉金斑蝶 *Danaus plexippus*, Pfeiler *et al.*, 2017)相似,同时也印证了小菜蛾的远距离迁移对于区域小菜蛾的基因交流的重要作用(Endersby *et al.*, 2006; Saw *et al.*, 2006; Wei *et al.*, 2013; Perry *et al.*, 2017)。群体中大部分个体选择停留在离出生地及其不远的地方,而其他一些个体则通过迁移一定的距离离开出生地(Lowe and McPeck, 2014)。这一生物学习性在物种栖息地扩张中有重要的作用(Lester *et al.*, 2007),同时也影响到当地群体的密

度以及物种间的相互作用(Koelle and Vandermeer, 2005)。与此同时,迁移促进了群体间的基因交流和混合(Moore *et al.*, 2017),在降低群体特异遗传变异的同时也提高了区域内群体总体的遗传变异水平(Wallberg *et al.*, 2014; Ke *et al.*, 2015),从而提高了群体应对外界环境压力(如气候变化, Aitken and Whitlock, 2013)的能力。迁移同时也促进了适应性遗传变异在群体间的交流(Herzig, 1995; Margaritopoulos *et al.*, 2009),有利于迁入群体快速适应新的选择压力(Tran *et al.*, 2007)。

#### 3.3 小菜蛾区域性防控的策略

在防治上,考虑到小菜蛾复合群体的特性,可以适时地进行“南北休耕轮作”(李振宇等, 2016);可选择在越冬区定期进行十字花科蔬菜和其他作物的轮作,这样会在一定程度上阻断群体适应性遗传变异的传递,同时也可阻断选择压力对害虫的持续选择作用,延缓适应性的形成;而对于季节性繁殖区域的群体,根据中国小菜蛾群体由南到北迁移高峰期为 6 月和 8 月(Fu *et al.*, 2014),可在这一时期内,在北方地区种植与十字花科蔬菜具有相同经济价值和市场需求的蔬菜和其他作物,以避免迁入群体高峰期,降低定殖虫口数量。

小菜蛾通过固有变异以及新的突变两种方式对化学农药进行快速适应(Hawkins *et al.*, 2019),是其难以防治并造成严重危害的重要因素。目前,小菜蛾已经对几乎所有用于防治的农药产生抗性(Furlong *et al.*, 2013),前人的研究已经获得了一系列抗性位点(Baxter *et al.*, 2011; Endersby *et al.*, 2011; Sonoda *et al.*, 2012; Guo *et al.*, 2014; Yan *et al.*, 2014; Yeh *et al.*, 2014; Liu *et al.*, 2015; Zhang *et al.*, 2015; Wang J *et al.*, 2016; Wang XL *et al.*, 2016)。根据我们的研究结果,小菜蛾在越冬区内,固有遗传变异的传递和新的遗传变异的积累将有利于小菜蛾对新的选择压力产生适应性,同时也使得抗性基因得以保留,并可能对其他化学农药产生交互抗性。在迁移群体中,这些抗性位点会随着小菜蛾的迁移进入新定殖的群体,这将加速迁入地群体抗药性的产生和发展。通过中性位点结合抗性基因的研究,不仅可以对小菜蛾迁移路径提供更加准确的分析,同时也能够为迁入地群体进行抗性以及交互抗性的预测预报。

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魏书军博士提供小菜蛾 *COI* 的原始数据。

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